

**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/001,039A**

DATE: 08/06/98

TIME: 12:40:51

INPUT SET: S27916.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Chiron Corporation

(ii) TITLE OF INVENTION: Methods for Administration of Recombinant Gene Delivery Vehicles for Treatment of Hemophilia and Other Disorders

(iii) NUMBER OF SEQUENCES: 83

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Chiron Corporation
(B) STREET: 4560 Horton Street
(C) CITY: Emeryville
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 94608

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kruse, Norman J.
(B) REGISTRATION NUMBER: 35,235
(C) REFERENCE/DOCKET NUMBER: 1155.005

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (510) 923-3520
(B) TELEFAX: (510) 655-3542

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pa.
(B) TYPE: nucleic acid

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47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: linear
49 (ii) MOLECULE TYPE: DNA (genomic)
50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
51 GAGAGATGGG GGAGGCTAAC TGAG

24

52
53 (2) INFORMATION FOR SEQ ID NO:2:
54 (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 28 base pairs
56 (B) TYPE: nucleic acid
57 (C) STRANDEDNESS: single
58 (D) TOPOLOGY: linear
59 (ii) MOLECULE TYPE: DNA (genomic)
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
61 GATCCTCAGT TAGCCTCCCC CATCTCTC

28

62
63 (2) INFORMATION FOR SEQ ID NO:3:
64 (i) SEQUENCE CHARACTERISTICS:
65 (A) LENGTH: 35 base pairs
66 (B) TYPE: nucleic acid
67 (C) STRANDEDNESS: single
68 (D) TOPOLOGY: linear
69 (ii) MOLECULE TYPE: DNA (genomic)
70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
71 TATATCTCCA GATGAGGTAC ATGATTTCAG GCTTG

35

72
73 (2) INFORMATION FOR SEQ ID NO:4:
74 (i) SEQUENCE CHARACTERISTICS:
75 (A) LENGTH: 40 base pairs
76 (B) TYPE: nucleic acid
77 (C) STRANDEDNESS: single
78 (D) TOPOLOGY: linear
79 (ii) MOLECULE TYPE: DNA (genomic)
80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
81 TATATATCGA TTCAAGGCAT TTTCTTTCA TCAATAAAAC

40

82
83 (2) INFORMATION FOR SEQ ID NO:5:
84 (i) SEQUENCE CHARACTERISTICS:
85 (A) LENGTH: 37 base pairs
86 (B) TYPE: nucleic acid
87 (C) STRANDEDNESS: single
88 (D) TOPOLOGY: linear
89 (ii) MOLECULE TYPE: DNA (genomic)
90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
91 TCGAGGATCC GCCCGGGCGG CCGCATCGAT GTCGACG

37

92
93 (2) INFORMATION FOR SEQ ID NO:6:
94 (i) SEQUENCE CHARACTERISTICS:
95 (A) LENGTH: 35 base pairs
96 (B) TYPE: nucleic acid
97 (C) STRANDEDNESS: single
98 (D) TOPOLOGY: linear
99 (ii) MOLECULE TYPE: DNA (genomic)

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100 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
101 CGCGTCGACA TCGATGCGGC CGCCCGGGCG GATCC
102
103
104 (2) INFORMATION FOR SEQ ID NO:7:
105 (i) SEQUENCE CHARACTERISTICS:
106 (A) LENGTH: 77 base pairs
107 (B) TYPE: nucleic acid
108 (C) STRANDEDNESS: single
109 (D) TOPOLOGY: linear
110 (ii) MOLECULE TYPE: DNA (genomic)
111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
112 AGTGAATTCTG AGCTCGGTAC CCGGGGATCC TCTAGAGTCG ACCTGCAGGC ATGCAAGCTT
113 GGC GTAATCA TGGTCAT
114
115 (2) INFORMATION FOR SEQ ID NO:8:
116 (i) SEQUENCE CHARACTERISTICS:
117 (A) LENGTH: 8 amino acids
118 (B) TYPE: amino acid
119 (C) STRANDEDNESS: single
120 (D) TOPOLOGY: linear
121 (ii) MOLECULE TYPE: protein
122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
123 Ala Arg Glu Met Gly Glu Ala Asn
124 1 5
125
126 (2) INFORMATION FOR SEQ ID NO:9:
127 (i) SEQUENCE CHARACTERISTICS:
128 (A) LENGTH: 27 base pairs
129 (B) TYPE: nucleic acid
130 (C) STRANDEDNESS: single
131 (D) TOPOLOGY: linear
132 (ii) MOLECULE TYPE: DNA (genomic)
133 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
134 CCCGAGAGAT GGGGGAGGCT AACTGAG
135
136 (2) INFORMATION FOR SEQ ID NO:10:
137 (i) SEQUENCE CHARACTERISTICS:
138 (A) LENGTH: 31 base pairs
139 (B) TYPE: nucleic acid
140 (C) STRANDEDNESS: single
141 (D) TOPOLOGY: linear
142 (ii) MOLECULE TYPE: DNA (genomic)
143 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
144 GGGCTCTCTA CCCCTCCGA TTGACACCTA G
145
146 (2) INFORMATION FOR SEQ ID NO:11:
147 (i) SEQUENCE CHARACTERISTICS:
148 (A) LENGTH: 5 amino acids
149 (B) TYPE: amino acid
150 (C) STRANDEDNESS: single
151 (D) TOPOLOGY: linear
152 (ii) MOLECULE TYPE: protein

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153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
154 Thr Ile Met Thr Met
155 1 5
156
157
158 (2) INFORMATION FOR SEQ ID NO:12:
159 (i) SEQUENCE CHARACTERISTICS:
160 (A) LENGTH: 24 base pairs
161 (B) TYPE: nucleic acid
162 (C) STRANDEDNESS: single
163 (D) TOPOLOGY: linear
164 (ii) MOLECULE TYPE: DNA (genomic)
165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
166 CCCTGTGCCT TATTTGAAC AACCC 24
167
168 (2) INFORMATION FOR SEQ ID NO:13:
169 (i) SEQUENCE CHARACTERISTICS:
170 (A) LENGTH: 24 base pairs
171 (B) TYPE: nucleic acid
172 (C) STRANDEDNESS: single
173 (D) TOPOLOGY: linear
174 (ii) MOLECULE TYPE: DNA (genomic)
175 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
176 CCCACCAACAA CCACATATCC CTCC 24
177
178 (2) INFORMATION FOR SEQ ID NO:14:
179 (i) SEQUENCE CHARACTERISTICS:
180 (A) LENGTH: 19 base pairs
181 (B) TYPE: nucleic acid
182 (C) STRANDEDNESS: single
183 (D) TOPOLOGY: linear
184 (ii) MOLECULE TYPE: DNA (genomic)
185 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
186 CCAGTCCTCC GATTGACTG 19
187
188 (2) INFORMATION FOR SEQ ID NO:15:
189 (i) SEQUENCE CHARACTERISTICS:
190 (A) LENGTH: 8332 base pairs
191 (B) TYPE: nucleic acid
192 (C) STRANDEDNESS: single
193 (D) TOPOLOGY: linear
194 (ii) MOLECULE TYPE: DNA (genomic)
195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
196
197 GCGCCAGTCC TCCGATTGAC TGAGTCGCC GGGTACCCGT GTATCCAATA AACCCCTTTG 60
198
199 CAGTTGCATC CGACTTGTGG TCTCGCTGTT CCTTGGGAGG GTCTCCTCTG AGTGATTGAC 120
200
201 TACCCGTCAG CGGGGGTCTT TCATTTGGGG GCTCGTCCGG GATCGGGAGA CCCCTGCCCA 180
202
203 GGGACCACCG ACCCACCAAC GGGAGGTAAG CTGGCCAGCA ACTTATCTGT GTCTGTCCGA 240
204
205 TTGTCTAGTG TCTATGACTG ATTTTATGCG CCTGCGTCGG TACTAGTTAG CTAACCTAGCT 300

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206 CTGTATCTGG CGGACCCGTG GTGGAACTGA CGAGTTCGGA ACACCCGGCC GCAACCCTGG 360
207
208 GAGACGTCCC AGGGACTTCG GGGGCCGTTT TTGTGGCCCG ACCTGAGTCC AAAAATCCCG 420
209
210 ATCGTTTG ACTCTTTGGT GCACCCCCCT TAGAGGAGGG ATATGTGGTT CTGGTAGGAG 480
211
212 ACGAGAACCT AAAACAGTTC CGGCCTCCGT CTGAATTTC GCTTCGGTT TGGGACCGAA 540
213
214 GCCGCCGCCGC CGGTCTTGTC TGCTGCAGCA TCGTTCTGTG TTGTCTCTGT CTGACTGTGT 600
215
216 TTCTGTATTT GTCTGAGAAT ATGGGCCAGA CTGTTACAC TCCCTTAAGT TTGACCTTAG 660
217
218 GTCACTGGAA AGATGTCGAG CGGATCGCTC ACAACCAGTC GGTAGATGTC AAGAAGAGAC 720
219
220 GTTGGGTTAC CTTCTGCTCT GCAGAATGGC CAACCTTAA CGTCGGATGG CGCGAGACG 780
221
222 GCACCTTAA CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTCA CCTGGCCCGC 840
223
224 ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTGGCT TTTGACCCCC 900
225
226 CTCCCTGGGT CAAGCCCTTT GTACACCCCTA AGCCTCCGCC TCCTCTTCCT CCATCCGCC 960
227
228 CGTCTCTCCC CCTTGAACCT CCTCGTTCGA CCCCGCCTCG ATCCTCCCTT TATCCAGCCC 1020
229
230 TCACTCCTTC TCTAGGCGCC AAACCTAAAC CTCAAGTTCT TTCTGACAGT GGGGGGCCGC 1080
231
232 TCATCGACCT ACTTACAGAA GACCCCCCGC CTTATAGGGA CCCAAGACCA CCCCCCTCCG 1140
233
234 ACAGGGACGG AAATGGTGGA GAAGCGACCC CTGCGGGAGA GGCACCGGAC CCCTCCCCAA 1200
235
236 TGGCATCTCG CCTACGTGG AGACGGGAGC CCCCTGTGGC CGACTCCACT ACCTCGCAGG 1260
237
238 CATTCCCCCT CCGCGCAGGA GGAAACGGAC AGCTTCAATA CTGGCCGTT TCCTCTTCTG 1320
239
240 ACCTTTACAA CTGGAAAAAT AATAACCCCTT CTTTTCTGA AGATCCAGGT AAACTGACAG 1380
241
242 CTCTGATCGA GTCTGTTCTC ATCACCCATC AGCCCACCTG GGACGACTGT CAGCAGCTGT 1440
243
244 TGGGGACTCT GCTGACCGGA GAAGAAAAAC AACGGGTGCT CTTAGAGGCT AGAAAGGCGG 1500
245
246 TGCGGGCGA TGATGGCGC CCCACTCAAC TGCCCAATGA AGTCGATGCC GCTTTCCCC 1560
247
248 TCGAGCGCCC AGACTGGGAT TACACCACCC AGGCAGGTAG GAACCACCTA GTCCACTATC 1620
249
250 GCCAGTTGCT CCTAGCGGGT CTCCAAAAG CGGGCAGAAG CCCCACCAAT TTGGCCAAGG 1680
251
252 TAAAAGGAAT AACACAAGGG CCCAATGAGT CTCCCTCGGC CTTCTAGAG AGACTTAAGG 1740
253
254 AAGCCTATCG CAGGTACACT CCTTATGACC CTGAGGACCC AGGGCAAGAA ACTAATGTGT 1800
255
256 CTATGTCTT CATTGGCAG TCTGCCAG ACATTGGAG AAAGTTAGAG AGGTTAGAAG 1860
257
258

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SEQUENCE VERIFICATION REPORT
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Original Text